

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,557

DATE: 12/17/2001

TIME: 11:01:04

Input Set : A:\36739A.txt

Output Set: N:\CRF3\12172001\J006557.raw

ENTERED

3 <110> APPLICANT: King, George L.
 4 Abrahamson, Susan
 5 Pugsley, Michael
 7 <120> TITLE OF INVENTION: Modulation of Pericyte Proliferation
 9 <130> FILE REFERENCE: 27129/36739A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/006,557
 C--> 11 <141> CURRENT FILING DATE: 2001-12-03
 11 <150> PRIOR APPLICATION NUMBER: 60/250,542
 12 <151> PRIOR FILING DATE: 2000-12-01
 14 <160> NUMBER OF SEQ ID NOS: 15
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1813
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (31)..(1491)
 26 <223> OTHER INFORMATION:
 29 <220> FEATURE:
 30 <221> NAME/KEY: mat_peptide
 31 <222> LOCATION: (124)..(1491)
 32 <223> OTHER INFORMATION:
 35 <220> FEATURE:
 36 <221> NAME/KEY: misc_feature
 37 <223> OTHER INFORMATION: rBPI
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 41 caggccttga ggttttggca gctctggagg atg aga gag aac atg gcc agg ggc 54
 42 Met Arg Glu Asn Met Ala Arg Gly
 43 -30 -25
 45 cct tgc aac gcg ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata K02
 46 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
 47 -20 -15 -10
 49 ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc 150
 50 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
 51 -5 -1 1 5
 53 tcc cag aag ggc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg 198
 54 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
 55 10 15 20 25
 57 cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt 246
 58 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
 59 30 35 40
 61 aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac 294
 62 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
 63 45 50 55
 65 atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat 342
 66 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn

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67	60	65	70	
69	gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg	390		
70	Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly			
71	75	80	85	
73	aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac	438		
74	Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp			
75	90	95	100	105
77	ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt	486		
78	Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser			
79	110	115	120	
81	aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc	534		
82	Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser			
83	125	130	135	
85	cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg	582		
86	His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp			
87	140	145	150	
89	ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag	630		
90	Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys			
91	155	160	165	
93	atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag	678		
94	Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys			
95	170	175	180	185
97	ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct	726		
98	Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser			
99	190	195	200	
101	gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct	774		
102	Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala			
103	205	210	215	
105	gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac	822		
106	Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His			
107	220	225	230	
109	cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc	870		
110	His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala			
111	235	240	245	
113	cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca	918		
114	His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr			
115	250	255	260	265
117	gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga	966		
118	Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg			
119	270	275	280	
121	gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc	1014		
122	Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe			
123	285	290	295	
125	ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag	1062		
126	Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys			
127	300	305	310	
129	ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag	1110		
130	Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln			
131	315	320	325	

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133 ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc      1158
134 Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala
135 330                               335                               340                               345
137 gtc ctc ccc aac tcc tcc ctg gct tcc ctc ttc ctg att ggc atg cac      1206
138 Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
139                               350                               355                               360
141 aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga      1254
142 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
143                               365                               370                               375
145 gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att      1302
146 Glu Leu Lys Leu Asp Arg Leu Leu Leu Glu Leu Lys His Ser Asn Ile
147                               380                               385                               390
149 ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta      1350
150 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
151                               395                               400                               405
153 ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc      1398
154 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
155 410                               415                               420                               425
157 cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag      1446
158 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
159                               430                               435                               440
161 cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa      1491
162 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
163                               445                               450                               455
165 tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttcctgatgg gctgtggggc      1551
167 accggtgcc tttcccaggg gaatcctctc cagatcttaa ccaagagccc cttgcaaact      1611
169 tcttcgactc agattcagaa atgatctaaa cagcaggaaa cattattcat tggaaaagtg      1671
171 catggtgtgt attttagggg ttatgagctt ctttcaaggg ctaaggctgc agagatatatt      1731
173 cctccaggaa tcgtgtttca attgtaacca agaaatttcc atttgtgctt catgaaaaaa      1791
175 aacttctggt ttttttcatg tg                                          1813
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179 <211> LENGTH: 487
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <223> OTHER INFORMATION: rBPI
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193 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
194  -15                               -10                               -5                               -1   1
197 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
198           5                               10                               15
201 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
202           20                               25                               30
205 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
206           35                               40                               45
209 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser

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210 50                               55                               60                               65
213 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
214                               70                               75                               80
217 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
218                               85                               90                               95
221 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
222                               100                              105                              110
225 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
226                               115                              120                              125
229 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
230 130                              135                              140                              145
233 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
234                               150                              155                              160
237 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
238                               165                              170                              175
241 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
242                               180                              185                              190
245 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
246                               195                              200                              205
249 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
250 210                              215                              220                              225
253 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
254                               230                              235                              240
257 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
258                               245                              250                              255
261 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
262                               260                              265                              270
265 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
266                               275                              280                              285
269 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
270 290                              295                              300                              305
273 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
274                               310                              315                              320
277 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
278                               325                              330                              335
281 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
282                               340                              345                              350
285 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
286                               355                              360                              365
289 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
290 370                              375                              380                              385
293 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
294                               390                              395                              400
297 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
298                               405                              410                              415
301 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
302                               420                              425                              430
305 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
306                               435                              440                              445

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309 Gly Ala Asp Val Val Tyr Lys
310 450                               455
313 <210> SEQ ID NO: 3
314 <211> LENGTH: 11
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <220> FEATURE:
319 <221> NAME/KEY: MISC_FEATURE
320 <223> OTHER INFORMATION: XMP.679
323 <220> FEATURE:
324 <221> NAME/KEY: SITE
325 <222> LOCATION: (5)..(5)
326 <223> OTHER INFORMATION: /label=Substituted-Ala note=position 5 is 1- naph-ala
329 <220> FEATURE:
330 <221> NAME/KEY: SITE
331 <222> LOCATION: (9)..(9)
332 <223> OTHER INFORMATION: /label=Substituted-Ala note=position 9 is 1- naph-ala
335 <220> FEATURE:
336 <221> NAME/KEY: SITE
337 <222> LOCATION: (1)..(11)
338 <223> OTHER INFORMATION: /Label=D Amino Acids/note=Positions 1-11 are D-Amino Acids
341 <220> FEATURE:
342 <221> NAME/KEY: SITE
343 <222> LOCATION: (11)..(11)
344 <223> OTHER INFORMATION: AMIDATION /label=Amidation note=The C-terminus is Amidated
347 <400> SEQUENCE: 3
349 Lys Leu Phe Lys Ala Gln Ala Lys Ala Lys Gly
350 1                               5..          10
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354 <211> LENGTH: 11
355 <212> TYPE: PRT
356 <213> ORGANISM: Homo sapiens
358 <220> FEATURE:
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360 <223> OTHER INFORMATION: XMP.627
363 <220> FEATURE:
364 <221> NAME/KEY: SITE
365 <222> LOCATION: (5)..(5)
366 <223> OTHER INFORMATION: /label=Substituted Ala note=position 5 is 1-naph-ala
369 <220> FEATURE:
370 <221> NAME/KEY: SITE
371 <222> LOCATION: (9)..(9)
372 <223> OTHER INFORMATION: /label=Substituted Ala note=position 9 is 1- naph-ala
375 <220> FEATURE:
376 <221> NAME/KEY: SITE
377 <222> LOCATION: (1)..(11)
378 <223> OTHER INFORMATION: /Label=D Amino Acids/note=Positions 1-11 are D-amino acids
381 <220> FEATURE:
382 <221> NAME/KEY: SITE

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VERIFICATION SUMMARY

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Input Set : A:\36739A.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date